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FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000
Please cite:
W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448


/tmp/fastaKAARTa4pQ: 1093 aa
 >Lex 177 SEQ ID NO:(4) human semaphorin
 vs  /tmp/fastaLAASTa4pQ library
searching /tmp/fastaLAASTa4pQ library


   1049 residues in       1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
 join: 39, opt: 27, gap-pen: -12/ -2, width:  16
 Scan time:  0.050
The best scores are:                                        opt
Lex 177 SEQ ID NO:(2) human semaphorin
               (1049) 7485


>>Lex 177 SEQ ID NO:2 human semaphorin
                   (1049 aa)
 initn: 7483 init1: 7483 opt: 7485
Smith-Waterman score: 7485;  99.904% identity in 1043 aa overlap (51-1093:7-1049)


            30        40        50        60        70        80
Lex     SHLSSSQDVSSEPSSEQQLCALSKHPTVAFEDLQPWVSNFTYPGARDFSQLALDPSGNQL
                           .:::::::::::::::::::::::::::::::::::
Lex                        MTVVNPQDLQPWVSNFTYPGARDFSQLALDPSGNQL
                               10        20        30


            90       100       110       120       130       140
Lex     IVGARNYLFRLSLANVSLLQATEWASSEDTRRSCQSKGKTEEECQNYVRVLIVAGRKVFM
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex     IVGARNYLFRLSLANVSLLQATEWASSEDTRRSCQSKGKTEEECQNYVRVLIVAGRKVFM
           40        50        60        70        80        90


           150       160       170       180       190       200
Lex     CGTNAFSPMCTSRQVGNLSRTIEKINGVARCPYDPRHNSTAVISSQGELYAATVIDFSGR
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex     CGTNAFSPMCTSRQVGNLSRTIEKINGVARCPYDPRHNSTAVISSQGELYAATVIDFSGR
          100       110       120       130       140       150


           210       220       230       240       250       260
Lex     DPAIYRSLGSGPPLRTAQYNSKWLNEPNFVAAYDIGLFAYFFLRENAVEHDCGRTVYSRV
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex     DPAIYRSLGSGPPLRTAQYNSKWLNEPNFVAAYDIGLFAYFFLRENAVEHDCGRTVYSRV
          160       170       180       190       200       210


           270       280       290       300       310       320
Lex     ARVCKNDVGGRFLLEDTWTTFMKARLNCSRPGEVPFYYNELQSAFHLPEQDLIYGVFTTN
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex     ARVCKNDVGGRFLLEDTWTTFMKARLNCSRPGEVPFYYNELQSAFHLPEQDLIYGVFTTN
          220       230       240       250       260       270


           330       340       350       360       370       380
Lex     VNSIAASAVCAFNLSAISQAFNGPFRYQENPRAAWLPIANPIPNFQCGTLPETGPNENLT
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex     VNSIAASAVCAFNLSAISQAFNGPFRYQENPRAAWLPIANPIPNFQCGTLPETGPNENLT
          280       290       300       310       320       330
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            390       400       410       420       430       440
Lex   ERSLQDAQRLFLMSEAVQPVTPEPCVTQDSVRFSHLVVDLVQAKDTLYHVLYIGTESGTI
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex   ERSLQDAQRLFLMSEAVQPVTPEPCVTQDSVRFSHLVVDLVQAKDTLYHVLYIGTESGTI
       340       350       360       370       380       390


            450       460       470       480       490       500
Lex   LKALSTASRSLHGCYLEELHVLPPGRREPLRSLRILHSARALFVGLRDGVLRVPLERCAA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex   LKALSTASRSLHGCYLEELHVLPPGRREPLRSLRILHSARALFVGLRDGVLRVPLERCAA
        400       410       420       430       440       450


            510       520       530       540       550       560
Lex   YRSQGACLGARDPYCGWDGKQQRCSTLEDSSNMSLWTQNITACPVRNVTRDGGFGPWSPW
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex   YRSQGACLGARDPYCGWDGKQQRCSTLEDSSNMSLWTQNITACPVRNVTRDGGFGPWSPW
        460       470       480       490       500       510


            570       580       590       600       610       620
Lex   QPCEHLDGDNSGSCLCRARSCDSPRPRCGGLDCLGPAIHIANCSRNGAWTPWSSWALCST
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex   QPCEHLDGDNSGSCLCRARSCDSPRPRCGGLDCLGPAIHIANCSRNGAWTPWSSWALCST
        520       530       540       550       560       570


            630       640       650       660       670       680
Lex   SCGIGFQVRQRSCSNPAPRHGGRICVGKSREERFCNENTPCPVPIFWASWGSWSKCSSNC
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex   SCGIGFQVRQRSCSNPAPRHGGRICVGKSREERFCNENTPCPVPIFWASWGSWSKCSSNC
        580       590       600       610       620       630


            690       700       710       720       730       740
Lex   GGGMQSRRRACENGNSCLGCGVEFKTCNPEGCPEVRRNTPWTPWLPVNVTQGGARQEQRF
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex   GGGMQSRRRACENGNSCLGCGVEFKTCNPEGCPEVRRNTPWTPWLPVNVTQGGARQEQRF
        640       650       660       670       680       690


            750       760       770       780       790       800
Lex   RFTCRAPLADPHGLQFGRRRTETRTCPADGSGSCDTDALVEDLLRSGSTSPHTVSGGWAA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex   RFTCRAPLADPHGLQFGRRRTETRTCPADGSGSCDTDALVEDLLRSGSTSPHTVSGGWAA
        700       710       720       730       740       750


            810       820       830       840       850       860
Lex   WGPWSSCSRDCELGFRVRKRTCTNPEPRNGGLPCVGDAAEYQDCNPQACPVRGAWSCWTS
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex   WGPWSSCSRDCELGFRVRKRTCTNPEPRNGGLPCVGDAAEYQDCNPQACPVRGAWSCWTS
        760       770       780       790       800       810


            870       880       890       900       910       920
Lex   WSPCSASCGGGHYQRTRSCTSPAPSPGEDICLGLHTEEALCATQACPEGWSPWSEWSKCT
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex   WSPCSASCGGGHYQRTRSCTSPAPSPGEDICLGLHTEEALCATQACPEGWSPWSEWSKCT
        820       830       840       850       860       870


            930       940       950       960       970       980
Lex   DDGAQSRSRHCEELLPGSSACAGNSSQSRPCPYSEIPVILPASSMEEATGCAGFNLIHLV
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex   DDGAQSRSRHCEELLPGSSACAGNSSQSRPCPYSEIPVILPASSMEEATGCAGFNLIHLV
        880       890       900       910       920       930
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              990        1000       1010       1020       1030       1040
Lex      ATGISCFLGSGLLTLAVYLSCQHCQRQSQESTLVHPATPNHLHYKGGGTPKNEKYTPMEF
         ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex      ATGISCFLGSGLLTLAVYLSCQHCQRQSQESTLVHPATPNHLHYKGGGTPKNEKYTPMEF
           940        950        960        970        980        990


             1050       1060       1070       1080       1090
Lex      KTLNKNNLIPDDRANFYPLQQTNVYTTTYYPSPLNKHSFRPEASPGQRCFPNS
         :::::::::::::::::::::::::::::::::::::::::::::::::::::::
Lex      KTLNKNNLIPDDRANFYPLQQTNVYTTTYYPSPLNKHSFRPEASPGQRCFPNS
           1000       1010       1020       1030       1040
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1093 residues in 1 query    sequences
1049 residues in 1 library sequences
 Scomplib [version 3.3t05 March 30, 2000]
 start: Wed Oct 29 10:33:25 2003 done: Wed Oct 29 10:33:26 2003
 Scan time:  0.050 Display time:  1.567

Function used was FASTA
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